The pattern of antibiotic resistance and determining of global QRDR area mutations on Fluoroquinolones resistance in Shigella species isolated from patients referred to Bou-Ali hospital of Ardabil 1393-1395

Background and Objective: Fluoroquinolones have been used successfully in recent years for the treatment of shigellosis, but mutations in the gyrA and parC genes in the QRDR gene location is the main mechanisms for producing resistance to Fluoroquinolones in the strains.This study was conducted to evaluate the antibiotic resistance pattern and consider the mutations in strains with resistance to Fluoroquinolones.

Methods: This study was performed on 113 clinical isolated Shigella from 1280 patients referred to the laboratory of Bu-Ali hospital in Ardabil.

Fecal samples were cultured in XLD and Hekton Enteric agar for the isolation of *Shigella* spp, which were identified biochemically by the standard methods, and grouped serologically by slide agglutination with specific antiseras. Evaluation of antibiotic resistance patterns performed by Kirby-bauer method and MIC determination.The last step was evaluating the mutations in strains with resistance to Fluoroquinolones by determining the sequence of resistance regions against Fluoroquinolones in the gyrA and parC genes.

Result: The study showed that *Shigella sonnei* is the dominant serotype in the Ardabil area (69.9%). Antibiotic resistance pattern showed that it was the most resistant to Trimethoprim-Sulfamethoxazol (82%) and the least resistance to Imipeneme (100%sensitive). 51% of strains were resistant to Nalidixic acid and 4.4% of strains were resistant to Fluoroquinolones. The presence of ipaH gene in all strains, and rfc and wbgz in *Shigella flexneri* and *Shigella sonnei* strains, confirmed by PCR.

Of the 113 isolates, 5 cases were detected resistant to Fluoroquinolones. After determining the sequence, mutations were detected in both gyrA and parC genes. The main mutations were replaced Ser80 with Leu and Asp87 with Asn or Gly in gyrA gene and Ser80 replacement with Ile in parC gene.

Conclusion: The result of the study of gyrA and parC genes sequence shows the mutations that cause resistance to Fluoroquinolones, but none of this mutations were observed in susceptible strains

Key words:

Shigella, Antibiotic resistance, Fluoro-quinolone resistance, mutation, *gyrA* gene, *parC* gene